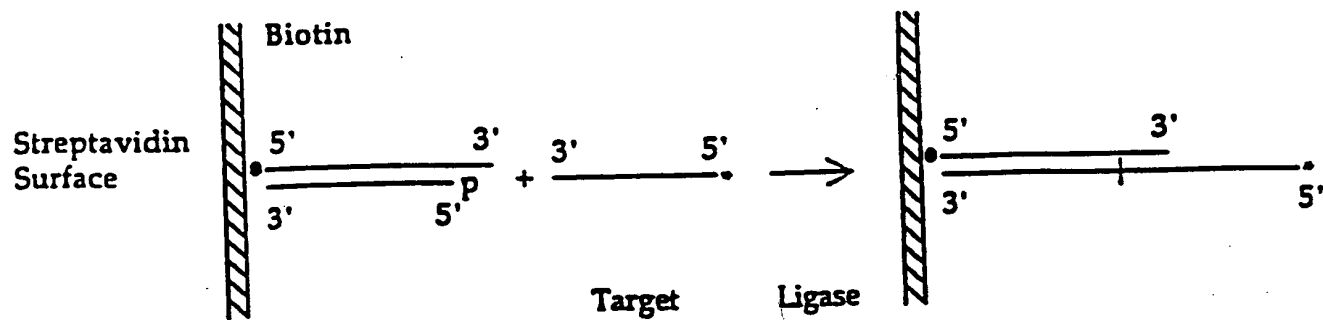


0003057.02490
 864220" T 250E060

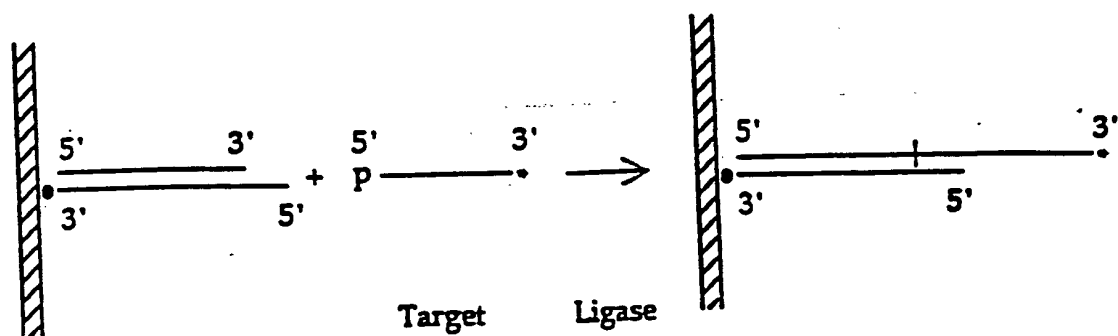
Nucleic Acid - Structure	Calculated T_m ($^{\circ}\text{C}$, average base composition)			
	n= 8	7	6	5
	38	33	25	15
	33	25	15	3
	25	15	3	-14
	51	46	40	31
	46	40	31	21
	40	31	21	11

FIGURE 1

Ligation of target DNA with probe



A



B.

FIGURE 3

0003057-02498

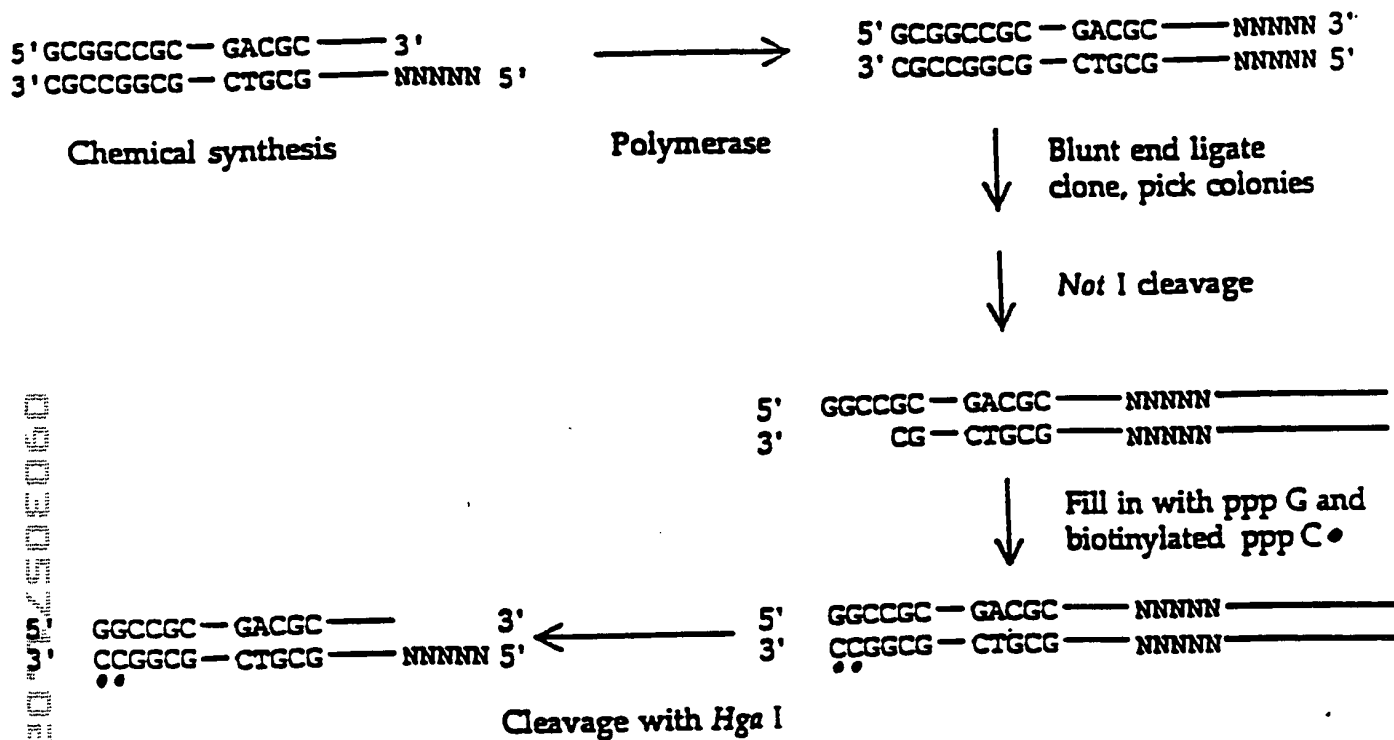
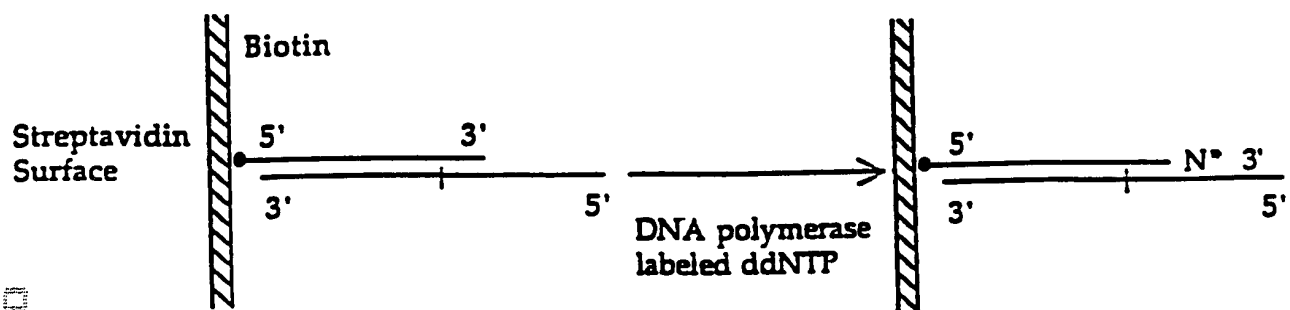


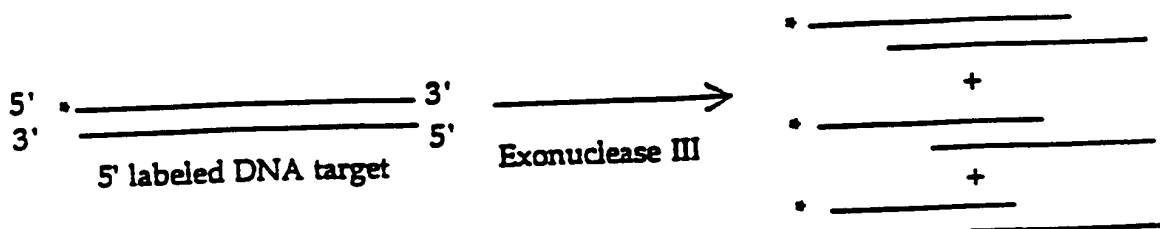
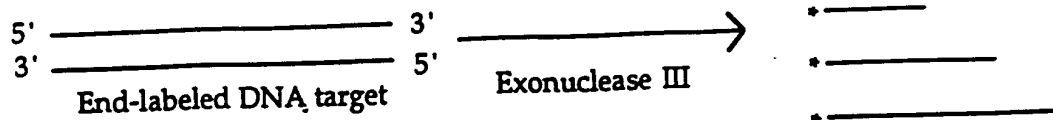
FIGURE 4

954220" T430E060



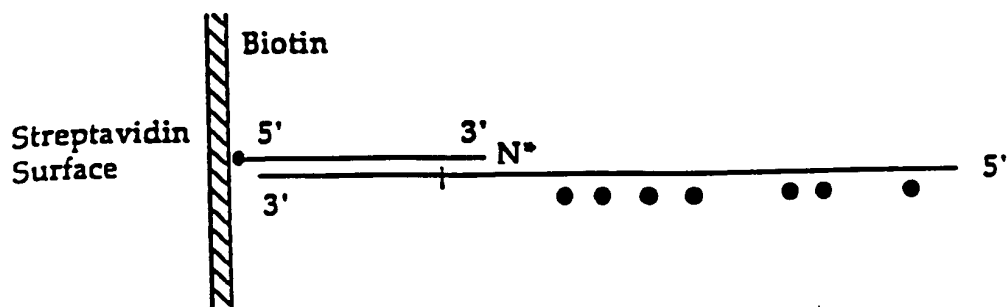
Reading an extra target base by 3' extension of the probe

FIGURE 5



Preparation of a nested set of DNAs

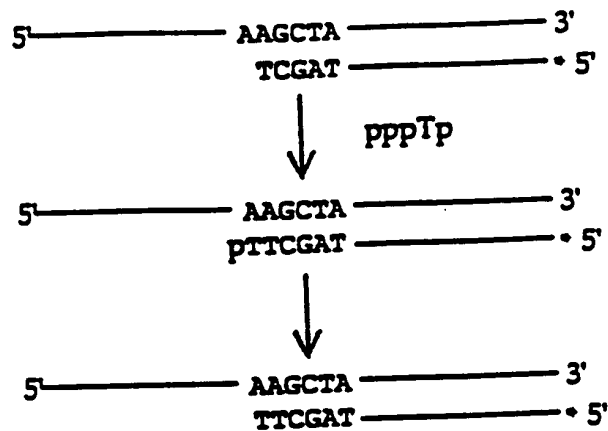
FIGURE 6



Positional information from ratio of internal label (●) to extension label (*). A 5' label could also be used.

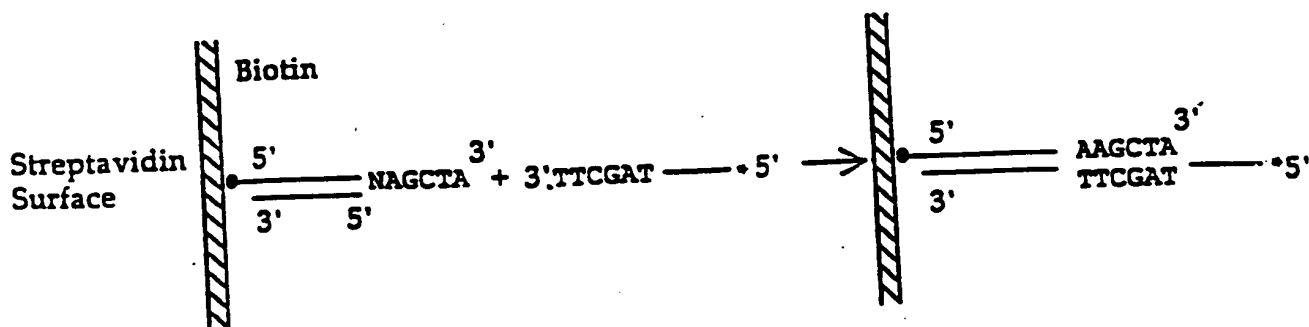
FIGURE 7

Reading an extra target base



Extension will fail with pppAp, pppGp, and pppCp

A. 3' extension of the target with a pppNp prior to phosphatase treatment



Array with one degenerate base

B. Hybridization and ligation

FIGURE 8

09030571-022498

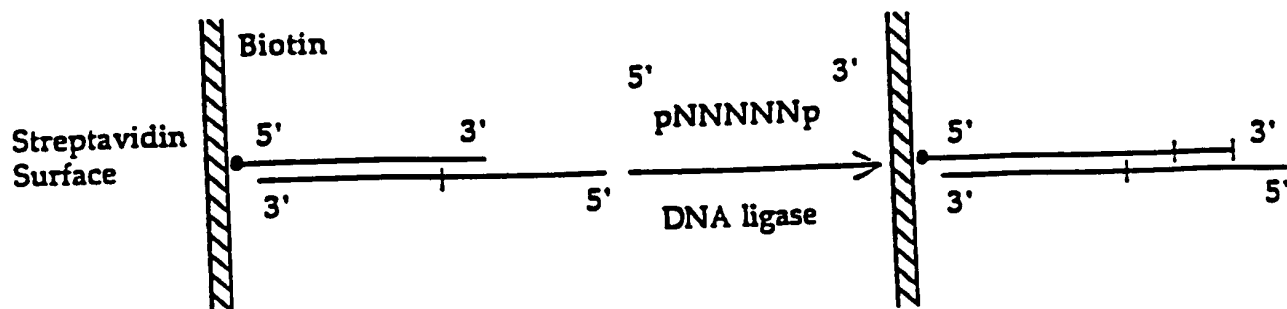
LABEL INTENSITY

Chain Terminator:	T	G	A
SEQUENCE			
GGAAT	2A, 2G	-	2G
AAGGT	2A, 2G	2A	-
GAAGT	2A, 2G	-	1G
AGGAT	2A, 2G	1A	-
AGAGT	2A, 2G	1A	-
GAGAT	2A, 2G	-	1G
GGGAT	1A, 3G	-	3G
GGAGT	1A, 3G	-	2G
GAGGT	1A, 3G	-	1G
AGGGT	1A, 3G	1A	-
AAAGT	3A, 1G	3A	-
AAGAT	3A, 1G	2A	-
AGAAT	3A, 1G	1A	-
GAAAT	3A, 1G	-	1G
GGGGT	4G	-	1T, 4G*
AAAAT	4A	1T, 4A*	-

Four color analysis of sequence extension of the 3' end of the probe. Label intensity shown does not include contribution from the 3' terminator.

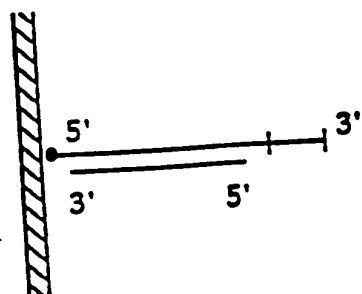
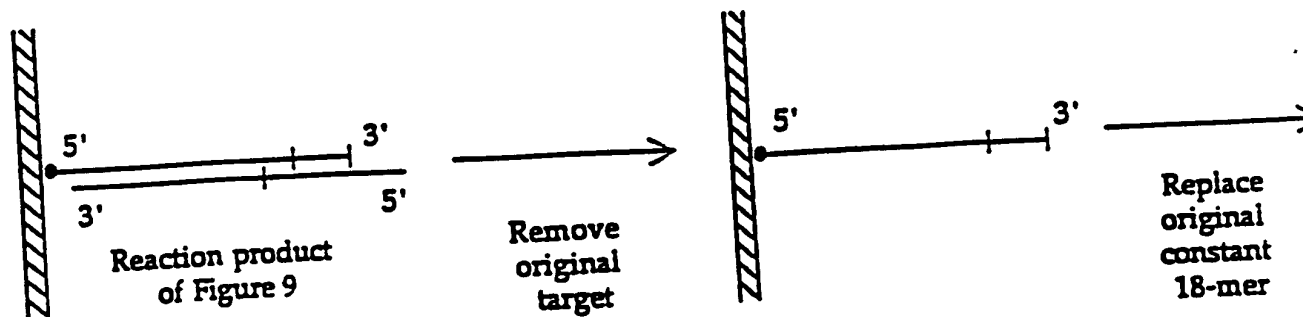
* Plus additional possible residues

FIGURE 9



Extension of the probe by ligation of a blocked pentanucleotide.
The pentanucleotide is 3'-blocked to prevent polymerization.

FIGURE 10



Preparation of a customized probe containing a 10 bp sequence present in the original target DNA

FIGURE 11

09030571-03458
364230-72505050

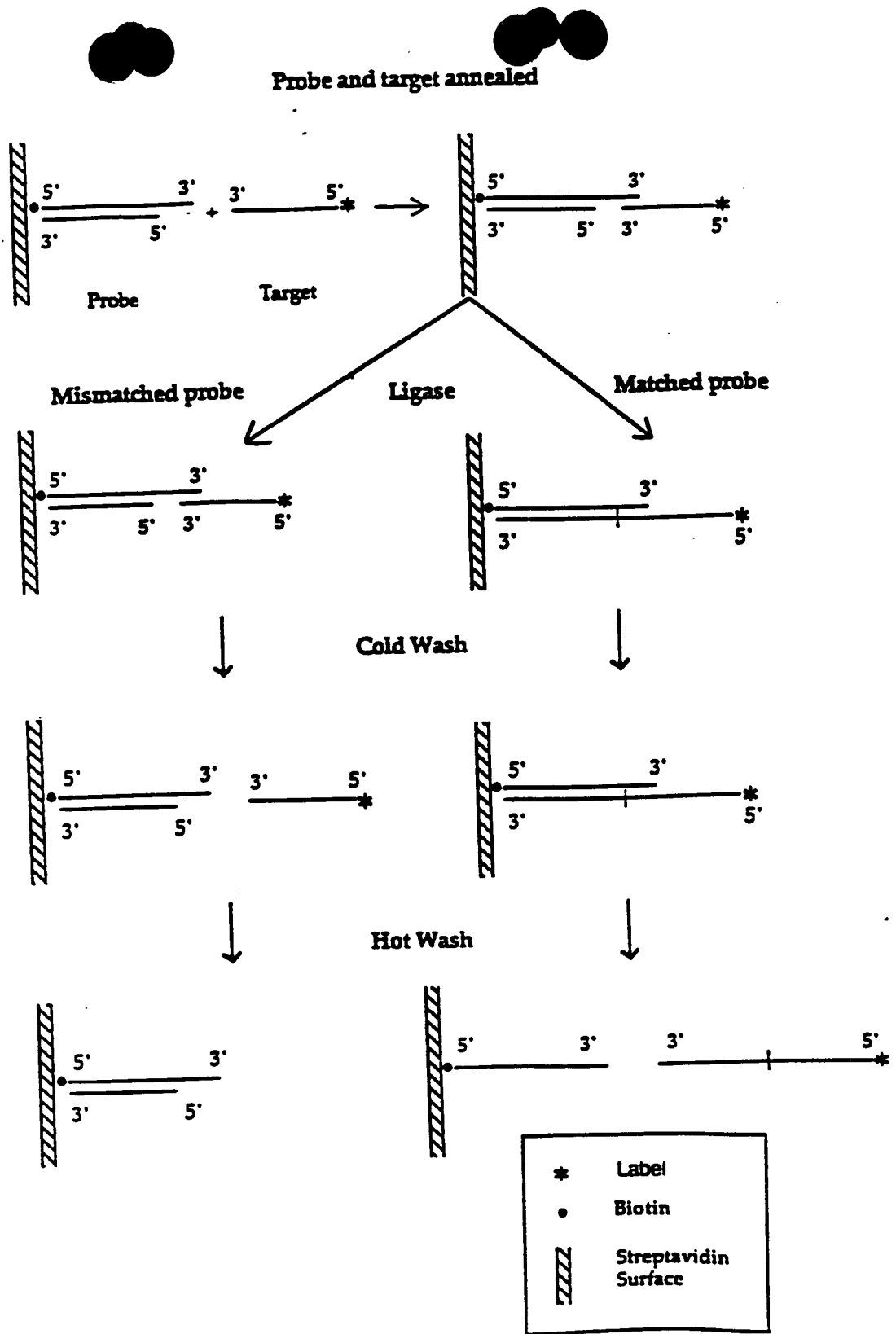


FIGURE 12

Ligation Efficiency

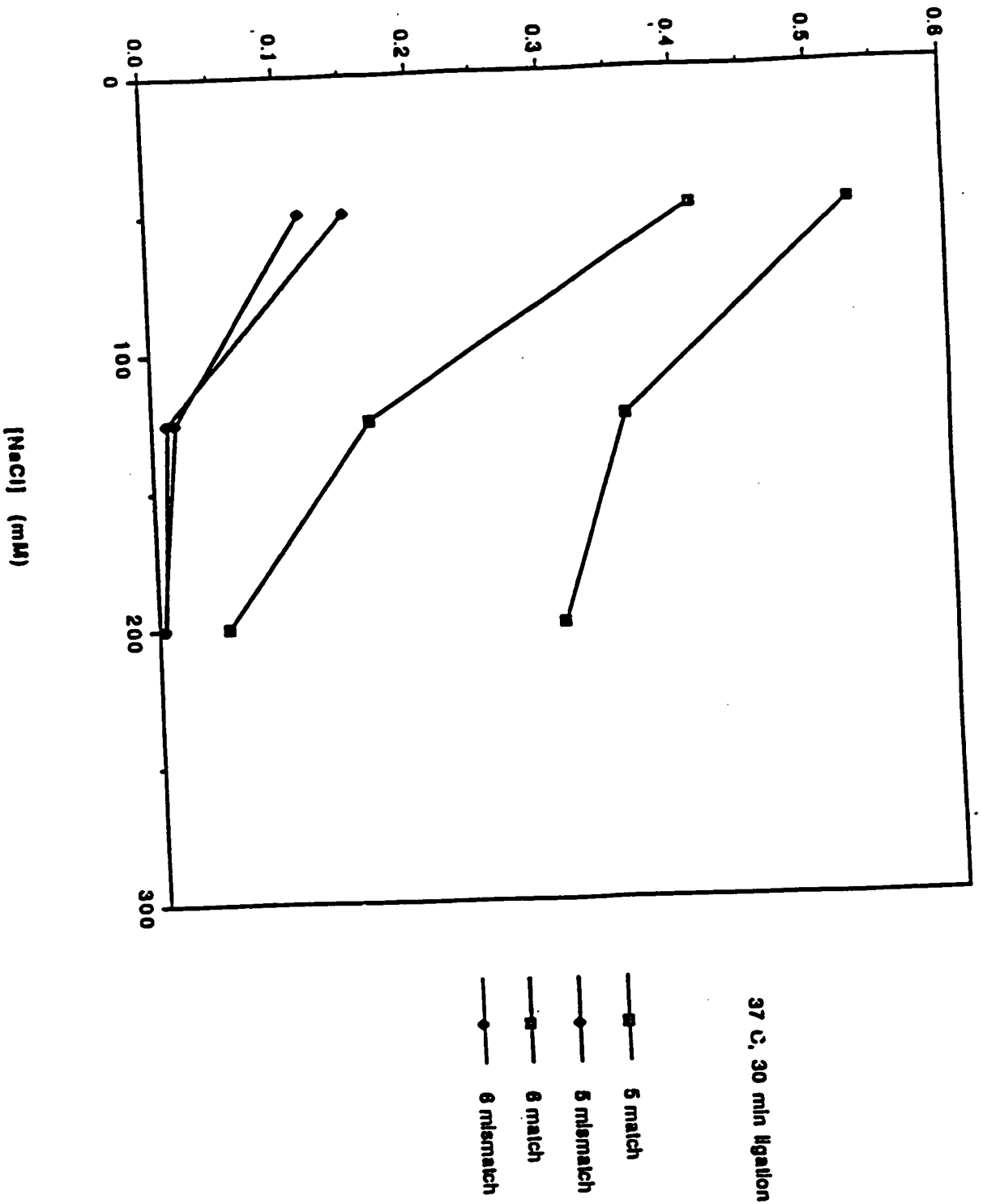


FIGURE 13

09030571.02249B

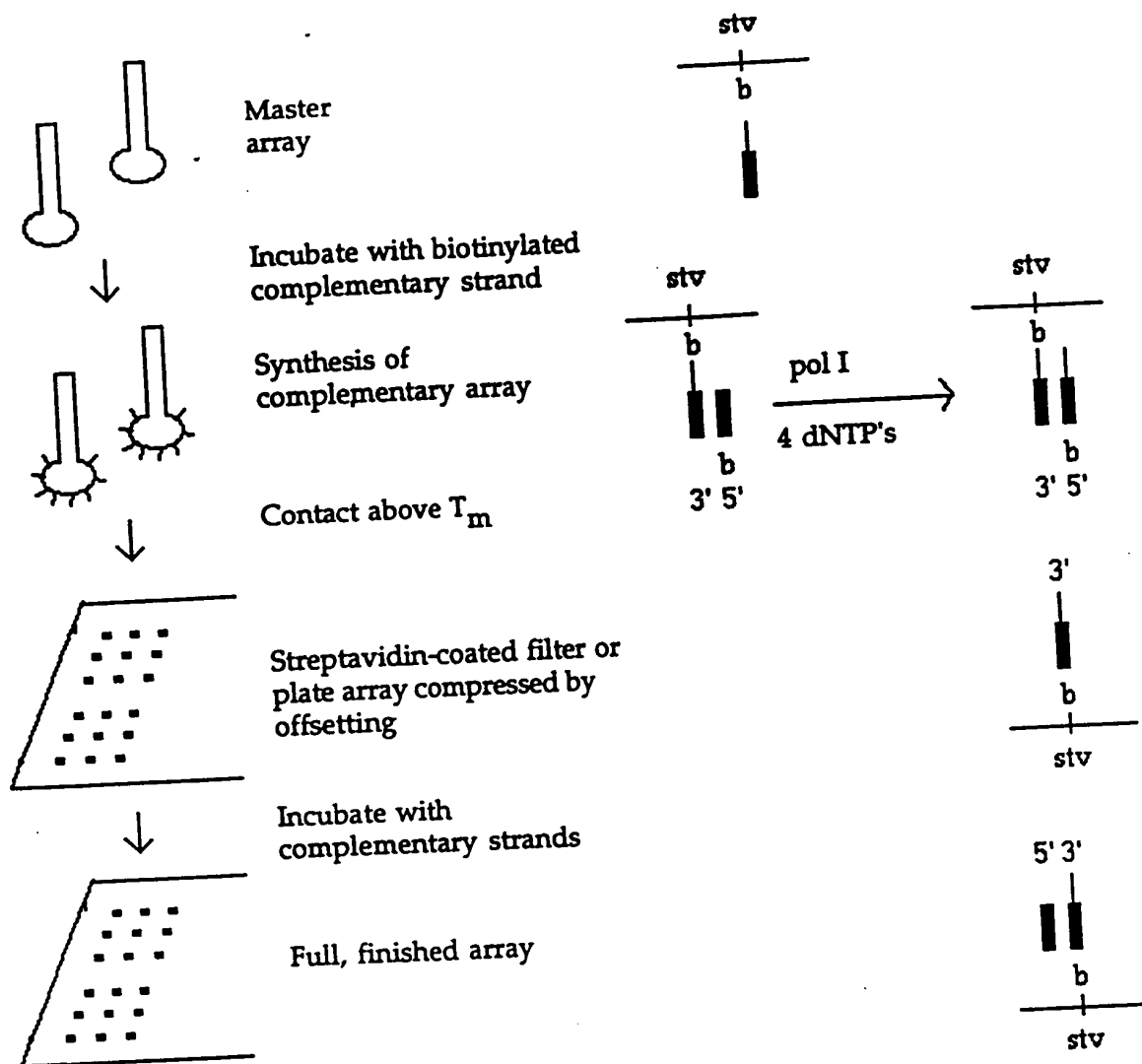


FIGURE 14